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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/016,686

DATE: 06/05/2002
TIME: 10:35:57

Input Set : A:\00069165.txt
Output Set: N:\CRF3\06052002\J016686.raw

ENTERED

3 <110> APPLICANT: Oxford Biomedica (UK) Limited
 4 Kingsman, Alan
 5 Kingsman, Susan Mary
 6 Bebbington, Christopher Robert
 7 Carroll, Miles William
 8 Ellard, Fiona Margaret
 9 Myers, Kevin Alan
 11 <120> TITLE OF INVENTION: Antibodies
 13 <130> FILE REFERENCE: 674523-2012
 15 <140> CURRENT APPLICATION NUMBER: 10/016,686
 C--> 16 <141> CURRENT FILING DATE: 2002-11-02
 18 <150> PRIOR APPLICATION NUMBER: PCT/GB00/04317
 19 <151> PRIOR FILING DATE: 2000-11-13
 21 <160> NUMBER OF SEQ ID NOS: 37
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 243
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: sequence of the mature secreted protein
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 36 1 5 10 15
 39 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
 40 20 25 30
 43 Tyr Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 44 35 40 45
 47 Gly Arg Ile Asn Pro Asn Asn Gly Val Thr Leu Tyr Asn Gln Lys Phe
 48 50 55 60
 51 Lys Asp Lys Ala Ile Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
 52 65 70 75 80
 55 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 56 85 90 95
 59 Ala Arg Ser Thr Met Ile Thr Asn Tyr Val Met Asp Tyr Trp Gly Gln .
 60 100 105 110
 63 Val Thr Ser Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
 64 115 120 125
 67 Gly Thr Gly Gly Gly Ser Ser Ile Val Met Thr Gln Thr Pro Thr
 68 130 135 140
 71 Phe Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr Cys Lys Ala
 72 145 150 155 160
 75 Ser Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly

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76 165 170 175
 79 Gln Ser Pro Thr Leu Leu Ile Ser Tyr Thr Ser Ser Arg Tyr Ala Gly
 80 180 185 190
 83 Val Pro Asp Arg Phe Ile Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe
 84 195 200 205
 87 Thr Ile Ser Thr Leu Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln
 88 210 215 220
 91 Gln Asp Tyr Asn Ser Pro Pro Thr Phe Gly Gly Thr Lys Leu Glu
 92 225 230 235 240
 95 Ile Lys Arg
 99 <210> SEQ ID NO: 2
 100 <211> LENGTH: 68
 101 <212> TYPE: DNA
 102 <213> ORGANISM: Artificial Sequence
 104 <220> FEATURE:
 105 <223> OTHER INFORMATION: Cassette 1- Translation initiation signal and signal peptide
 107 <400> SEQUENCE: 2
 108 aagcttccac catggatgg agctgtatca tcctcttctt ggttagcaaca gctacaggtg 60
 110 tccactcc 68
 113 <210> SEQ ID NO: 3
 114 <211> LENGTH: 488
 115 <212> TYPE: PRT
 116 <213> ORGANISM: Artificial Sequence
 118 <220> FEATURE:
 119 <223> OTHER INFORMATION: deduced amino acid sequence for the B7-1.5T4.1 fusion
 protein
 121 <400> SEQUENCE: 3
 123 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 124 1 5 10 15
 127 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
 128 20 25 30
 131 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
 132 35 40 45
 135 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
 136 50 55 60
 139 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
 140 65 70 75 80
 143 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
 144 85 90 95
 147 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
 148 100 105 110
 151 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
 152 115 120 125
 155 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
 156 130 135 140
 159 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
 160 145 150 155 160
 163 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
 164 165 170 175
 167 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp

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168	180	185	190
171	Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met		
172	195	200	205
175	Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg		
176	210	215	220
179	Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro		
180	225	230	235
183	Asp Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Asp		240
184	245	250	255
187	Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly		
188	260	265	270
191	Tyr Ser Phe Thr Gly Tyr Tyr Met His Trp Val Lys Gln Ser His Gly		
192	275	280	285
195	Lys Ser Leu Glu Trp Ile Gly Arg Ile Asn Pro Asn Asn Gly Val Thr		
196	290	295	300
199	Leu Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Leu Thr Val Asp Lys		
200	305	310	315
203	Ser Ser Thr Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp		320
204	325	330	335
207	Ser Ala Val Tyr Tyr Cys Ala Arg Ser Thr Met Ile Thr Asn Tyr Val		
208	340	345	350
211	Met Asp Tyr Trp Gly Gln Val Thr Ser Val Thr Val Ser Ser Gly Gly		
212	355	360	365
215	Gly Gly Ser Gly Gly Gly Thr Gly Gly Gly Ser Ser Ile Val		
216	370	375	380
219	Met Thr Gln Thr Pro Thr Phe Leu Leu Val Ser Ala Gly Asp Arg Val		
220	385	390	395
223	400	405	410
224	415		
227	Tyr Gln Gln Lys Pro Gly Gln Ser Pro Thr Leu Leu Ile Ser Tyr Thr		
228	420	425	430
231	Ser Ser Arg Tyr Ala Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Tyr		
232	435	440	445
235	Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Leu Gln Ala Glu Asp Leu		
236	450	455	460
239	Ala Val Tyr Phe Cys Gln Gln Asp Tyr Asn Ser Pro Pro Thr Phe Gly		
240	465	470	475
243	480		
244	Gly Gly Thr Lys Leu Glu Ile Lys		
244	485		
247	<210> SEQ ID NO: 4		
248	<211> LENGTH: 592		
249	<212> TYPE: PRT		
250	<213> ORGANISM: Artificial Sequence		
252	<220> FEATURE:		
253	<223> OTHER INFORMATION: deduced amino acid sequence for the Ig-5T4 fusion protein		
255	<400> SEQUENCE: 4		
257	Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly		
258	1	5	10
261	15		
	Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys		

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262	20	25	30	
265	Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe			
266	35	40	45	
269	Thr Gly Tyr Tyr Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu			
270	50	55	60	
273	Glu Trp Ile Gly Arg Ile Asn Pro Asn Asn Gly Val Thr Leu Tyr Asn			
274	65	70	75	80
277	Gln Lys Phe Lys Asp Lys Ala Ile Leu Thr Val Asp Lys Ser Ser Thr			
278	85	90	95	
281	Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val			
282	100	105	110	
285	Tyr Tyr Cys Ala Arg Ser Thr Met Ile Thr Asn Tyr Val Met Asp Tyr			
286	115	120	125	
289	Trp Gly Gln Val Thr Ser Val Thr Val Ser Ser Gly Gly Gly Ser			
290	130	135	140	
293	Gly Gly Gly Thr Gly Gly Ser Ser Ile Val Met Thr Gln			
294	145	150	155	160
297	Thr Pro Thr Phe Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr			
298	165	170	175	
301	Cys Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln			
302	180	185	190	
305	Lys Pro Gly Gln Ser Pro Thr Leu Leu Ile Ser Tyr Thr Ser Ser Arg			
306	195	200	205	
309	Tyr Ala Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Tyr Gly Thr Asp			
310	210	215	220	
313	Phe Thr Phe Thr Ile Ser Thr Leu Gln Ala Glu Asp Leu Ala Val Tyr			
314	225	230	235	240
317	Phe Cys Gln Gln Asp Tyr Asn Ser Pro Pro Thr Phe Gly Gly Thr			
318	245	250	255	
321	Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro			
322	260	265	270	
325	Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly			
326	275	280	285	
329	Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn			
330	290	295	300	
333	Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln			
334	305	310	315	320
337	Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser			
338	325	330	335	
341	Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser			
342	340	345	350	
345	Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr			
346	355	360	365	
349	His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser			
350	370	375	380	
353	Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg			
354	385	390	395	400
357	Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro			
358	405	410	415	

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361 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
362 420 425 430
365 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
366 435 440 445
369 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
370 450 455 460
373 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
374 465 470 475 480
377 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
378 485 490 495
381 Pro Pro Ser Arg Asp Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
382 500 505 510
385 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
386 515 520 525
389 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
390 530 535 540
393 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
394 545 550 555 560
397 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
398 565 570 575
401 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
402 580 585 590
405 <210> SEQ ID NO: 5
406 <211> LENGTH: 729
407 <212> TYPE: DNA
408 <213> ORGANISM: Artificial Sequence
410 <220> FEATURE:
411 <223> OTHER INFORMATION: DNA sequence encoding a 5T4 ScFv designated 5T4ScFv.1
413 <400> SEQUENCE: 5
414 gaggtccagc ttcagcagtc tggacctgac ctggtaagc ctggggcttc agtgaagata 60
416 tcctgcaagg cttctggta ctcattcact ggctactaca tgcactgggt gaagcagagc 120
418 catggaaaga gccttgagtg gattggacgt attaatccta acaatgggt tactctctac 180
420 aaccagaaat tcaaggacaa ggcattatata actgttagaca agtcatccac cacagcctac 240
422 atggagctcc gcagcctgac atctgaggac tctgcggctc attactgtgc aagatctact 300
424 atgattacga actatgttat ggactactgg ggtcaagtaa cctcagtac cgtctccctca 360
426 ggtggtggtg ggagcgggtgg tggcggcaact ggcggcggcg gatctagttat tgtgtatgacc 420
428 cagactccca cattcctgct tgtttcagca ggagacaggg ttaccataac ctgcaaggcc 480
430 agtcagagtg tgtagtaatga tggtagdttgg taccacacaga agccaggggca gtctcctaca 540
432 ctgctcatat cctatacatac cagtcgctac gctggagtcc ctgatcgctt cattggcagt 600
434 ggatatggga cggatttcac tttcaccatc agcactttgc aggctgaaga cctggcagtt 660
436 tatttcgttc agcaagatta taattctcct ccgacgttcg gtggaggcac caagctggaa 720
438 atcaaacgg 729
441 <210> SEQ ID NO: 6
442 <211> LENGTH: 43
443 <212> TYPE: DNA
444 <213> ORGANISM: Artificial Sequence
446 <220> FEATURE:
447 <223> OTHER INFORMATION: oligonucleotide used to construct flexible linker to join
the ext
448 racellular domain of B7.1 and ScFv

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/016,686

DATE: 06/05/2002

TIME: 10:35:58

Input Set : A:\00069165.txt

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